

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/476,798DATE: 03/26/96
TIME: 17:57:25

INPUT SET: S9549.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Deboer, Herman A.
Strijker, Rein
Heyneker, Herbert L.
Platenburg, Gerald
Lee, Sang He
Pieper, Frank
Krimpenfort, Paul J.A.

ENTERED

(ii) TITLE OF INVENTION: Production of Recombinant Polypeptides
by Bovine Species and Transgenic Methods

(iii) NUMBER OF SEQUENCES: 38

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Townsend and Townsend and Crew
(B) STREET: One Market Plaza, Steuart Tower, Suite 2000
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94105

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/476,798
(B) FILING DATE: 07-JUN-1995
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/077,788
(B) FILING DATE: 15-JUN-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/895,956
(B) FILING DATE: 15-JUN-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/619,131

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47 (B) FILING DATE: 27-NOV-1990
48
49 (vii) PRIOR APPLICATION DATA:
50 (A) APPLICATION NUMBER: US 07/444,745
51 (B) FILING DATE: 01-DEC-1989
52
53 (viii) ATTORNEY/AGENT INFORMATION:
54 (A) NAME: Liebescheutz, Joe O.
55 (B) REGISTRATION NUMBER: 37,505
56 (C) REFERENCE/DOCKET NUMBER: 16994-003125
57
58 (ix) TELECOMMUNICATION INFORMATION:
59 (A) TELEPHONE: 415-543-9600
60 (B) TELEFAX: 415-543-5043
61
62
63 (2) INFORMATION FOR SEQ ID NO:1:
64
65 (i) SEQUENCE CHARACTERISTICS:
66 (A) LENGTH: 2319 base pairs
67 (B) TYPE: nucleic acid
68 (C) STRANDEDNESS: single
69 (D) TOPOLOGY: linear
70
71 (ii) MOLECULE TYPE: DNA (genomic)
72
73
74 (ix) FEATURE:
75 (A) NAME/KEY: sig_peptide
76 (B) LOCATION: 1..54
77
78 (ix) FEATURE:
79 (A) NAME/KEY: mat_peptide
80 (B) LOCATION: 55..2130
81
82 (ix) FEATURE:
83 (A) NAME/KEY: CDS
84 (B) LOCATION: 1..2130
85
86
87 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
88
89 GGA CTT GTC TTC CTC GTC CTG CTG TTC CTC GGG GCC CTC GGA CTG TGT 48
90 Gly Leu Val Phe Leu Val Leu Leu Phe Leu Gly Ala Leu Gly Leu Cys
91 -18 -15 -10 -5
92
93 CTG GCT GGC CGT AGG AGA AGG AGT GTT CAG TGG TGC GCC GTA TCC CAA 96
94 Leu Ala Gly Arg Arg Arg Arg Ser Val Gln Trp Cys Ala Val Ser Gln
95 1 5 10
96
97 CCC GAG GCC ACA AAA TGC TTC CAA TGG CAA AGG AAT ATG AGA AAA GTG 144
98 Pro Glu Ala Thr Lys Cys Phe Gln Trp Gln Arg Asn Met Arg Lys Val
99 15 20 25 30

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100																		
101	CTG	GGC	CCT	CCT	GTC	AGC	TGC	ATA	AAG	AGA	GAC	TCC	CCC	ATC	CAG	TGT		192
102	Leu	Gly	Pro	Pro	Val	Ser	Cys	Ile	Lys	Arg	Asp	Ser	Pro	Ile	Gln	Cys		
103					35					40					45			
104																		
105	ATC	CAG	GCC	ATT	GCG	GAA	AAC	AGG	GCC	GAT	GCT	GTG	ACC	CTT	GAT	GGT		240
106	Ile	Gln	Ala	Ile	Ala	Glu	Asn	Arg	Ala	Asp	Ala	Val	Thr	Leu	Asp	Gly		
107				50					55					60				
108																		
109	GGT	TTC	ATA	TAC	GAG	GCA	GGC	CTG	GCC	CCC	TAC	AAA	CTG	CGA	CCT	GTA		288
110	Gly	Phe	Ile	Tyr	Glu	Ala	Gly	Leu	Ala	Pro	Tyr	Lys	Leu	Arg	Pro	Val		
111			65					70					75					
112																		
113	GCG	GCG	GAA	GTC	TAC	GGG	ACC	GAA	AGA	CAG	CCA	CGA	ACT	CAC	TAT	TAT		336
114	Ala	Ala	Glu	Val	Tyr	Gly	Thr	Glu	Arg	Gln	Pro	Arg	Thr	His	Tyr	Tyr		
115		80					85					90						
116																		
117	CGG	GTG	GCT	GTG	GTG	AAG	AAG	GGC	GGC	AGC	TTT	CAG	CTG	AAC	GAA	CTG		384
118	Arg	Val	Ala	Val	Val	Lys	Lys	Gly	Gly	Ser	Phe	Gln	Leu	Asn	Glu	Leu		
119	95					100					105					110		
120																		
121	CAA	GGT	CTG	AAG	TCC	TGC	CAC	ACA	GGC	CTT	CGC	AGG	ACC	GCT	GGA	TGG		432
122	Gln	Gly	Leu	Lys	Ser	Cys	His	Thr	Gly	Leu	Arg	Arg	Thr	Ala	Gly	Trp		
123					115					120					125			
124																		
125	AAT	GTC	CCT	ACA	GGG	ACA	CTT	CGT	CCA	TTC	TTG	AAT	TGG	ACG	GGT	CCA		480
126	Asn	Val	Pro	Thr	Gly	Thr	Leu	Arg	Pro	Phe	Leu	Asn	Trp	Thr	Gly	Pro		
127				130					135					140				
128																		
129	CCT	GAG	CCC	ATT	GAG	GCA	GCT	GTG	CAG	TTC	TTC	TCA	GCC	AGC	TGT	GTT		528
130	Pro	Glu	Pro	Ile	Glu	Ala	Ala	Val	Gln	Phe	Phe	Ser	Ala	Ser	Cys	Val		
131			145					150					155					
132																		
133	CCC	GGT	GCA	GAT	AAA	GGA	CAG	TTC	CCC	AAC	CTG	TGT	CGC	CTG	TGT	GCG		576
134	Pro	Gly	Ala	Asp	Lys	Gly	Gln	Phe	Pro	Asn	Leu	Cys	Arg	Leu	Cys	Ala		
135		160					165					170						
136																		
137	GGG	ACA	GGG	GAA	AAC	AAA	TGT	GCC	TTC	TCC	TCC	CAG	GAA	CCG	TAC	TTC		624
138	Gly	Thr	Gly	Glu	Asn	Lys	Cys	Ala	Phe	Ser</								

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153	GTG GAC AAG TTC AAA GAC TGC CAT CTG GCC CGG GTC CCT TCT CAT GCC	816
154	Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala	
155	240 245 250	
156		
157	GTT GTG GCA CGA AGT GTG AAT GGC AAG GAG GAT GCC ATC TGG AAT CTT	864
158	Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn Leu	
159	255 260 265 270	
160		
161	CTC CGC CAG GCA CAG GAA AAG TTT GGA AAG GAC AAG TCA CCG AAA TTC	912
162	Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys Phe	
163	275 280 285	
164		
165	CAG CTC TTT GGC TCC CCT AGT GGG CAG AAA GAT CTG CTG TTC AAG GAC	960
166	Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp	
167	290 295 300	
168		
169	TCT GCC ATT GGG TTT TCG AGG GTG CCC CCG AGG ATA GAT TCT GGG CTG	1008
170	Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu	
171	305 310 315	
172		
173	TAC CTT GGC TCC GGC TAC TTC ACT GCC ATC CAG AAC TTG AGG AAA AGT	1056
174	Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser	
175	320 325 330	
176		
177	GAG GAG GAA GTG GCT GCC CGG CGT GCG CGG GTC GTG TGG TGT GCG GTG	1104
178	Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala Val	
179	335 340 345 350	
180		
181	GGC GAG CAG GAG CTG CGC AAG TGT AAC CAG TGG AGT GGC TTG AGC GAA	1152
182	Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu	
183	355 360 365	
184		
185	GGC AGC GTG ACC TGC TCC TCG GCC TCC ACC ACA GAG GAC TGC ATC GCC	1200
186	Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala	
187	370 375 380	
188		
189	CTG GTG CTG AAA GGA GAA GCT GAT GCC ATG AGT TTG GAT GGA GGA TAT	1248
190	Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr	
191	385 390 395	
192		
193	GTG TAC ACT GCA TGC AAA TGT GGT TTG GTG CCT GTC CTG GCA GAG AAC	1296
194	Val Tyr Thr Ala Cys Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn	
195	400 405 410	
196		
197	TAC AAA TCC CAA CAA AGC AGT GAC CCT GAT CCT AAC TGT GTG GAT AGA	1344
198	Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg	
199	415 420 425 430	
200		
201	CCT GTG GAA GGA TAT CTT GCT GTG GCG GTG GTT AGG AGA TCA GAC ACT	1392
202	Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr	
203	435 440 445	
204		
205	AGC CTT ACC TGG AAC TCT GTG AAA GGC AAG AAG TCC TGC CAC ACC GCC	1440

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206	Ser	Leu	Thr	Trp	Asn	Ser	Val	Lys	Gly	Lys	Lys	Ser	Cys	His	Thr	Ala	
207				450					455					460			
208																	
209	GTG	GAC	AGG	ACT	GCA	GGC	TGG	AAT	ATC	CCC	ATG	GGC	CTG	CTC	TTC	AAC	1488
210	Val	Asp	Arg	Thr	Ala	Gly	Trp	Asn	Ile	Pro	Met	Gly	Leu	Leu	Phe	Asn	
211			465					470					475				
212																	
213	CAG	ACG	GGC	TCC	TGC	AAA	TTT	GAT	GAA	TAT	TTC	AGT	CAA	AGC	TGT	GCC	1536
214	Gln	Thr	Gly	Ser	Cys	Lys	Phe	Asp	Glu	Tyr	Phe	Ser	Gln	Ser	Cys	Ala	
215		480					485					490					
216																	
217	CCT	GGG	TCT	GAC	CCG	AGA	TCT	AAT	CTC	TGT	GCT	CTG	TGT	ATT	GGC	GAC	1584
218	Pro	Gly	Ser	Asp	Pro	Arg	Ser	Asn	Leu	Cys	Ala	Leu	Cys	Ile	Gly	Asp	
219	495					500					505					510	
220																	
221	GAG	CAG	GGT	GAG	AAT	AAG	TGC	GTG	CCC	AAC	AGC	AAT	GAG	AGA	TAC	TAC	1632
222	Glu	Gln	Gly	Glu	Asn	Lys	Cys	Val	Pro	Asn	Ser	Asn	Glu	Arg	Tyr	Tyr	
223					515					520					525		
224																	
225	GGC	TAC	ACT	GGG	GCT	TTC	CGG	TGC	CTG	GCT	GAG	AAT	GCT	GGA	GAC	GTT	1680
226	Gly	Tyr	Thr	Gly	Ala	Phe	Arg	Cys	Leu	Ala	Glu	Asn	Ala	Gly	Asp	Val	
227				530					535					540			
228																	
229	GCA	TTT	GTG	AAA	GAT	GTC	ACT	GTC	TTG	CAG	AAC	ACT	GAT	GGA	AAT	AAC	1728
230	Ala	Phe	Val	Lys	Asp	Val	Thr	Val	Leu	Gln	Asn	Thr	Asp	Gly	Asn	Asn	
231			545					550					555				
232																	
233	AAT	GAG	GCA	TGG	GCT	AAG	GAT	TTG	AAG	CTG	GCA	GAC	TTT	GCG	CTG	CTG	1776
234	Asn	Glu	Ala	Trp	Ala	Lys	Asp	Leu	Lys	Leu	Ala	Asp	Phe	Ala	Leu	Leu	
235		560					565					570					
236																	
237	TGC	CTC	GAT	GGC	AAA	CGG	AAG	CCT	GTG	ACT	GAG	GCT	AGA	AGC	TGC	CAT	1824
238	Cys	Leu	Asp	Gly	Lys	Arg	Lys	Pro	Val	Thr	Glu	Ala	Arg	Ser	Cys	His	
239	575					580					585					590	
240																	
241	CTT	GCC	ATG	GCC	CCG	AAT	CAT	GCC	GTG	GTG	TCT	CGG	ATG	GAT	AAG	GTG	1872
242	Leu	Ala	Met	Ala	Pro	Asn	His	Ala	Val	Val	Ser	Arg	Met	Asp	Lys	Val	
243					595					600					605		
244																	
245	GAA	CGC	CTG	AAA	CAG	GTG	CTG	CTC	CAC	CAA	CAG	GCT	AAA	TTT	GGG	AGA	1920
246	Glu	Arg	Leu	Lys	Gln	Val	Leu	Leu	His	Gln	Gln	Ala	Lys	Phe	Gly	Arg	
247				610					615					620			
248																	
249	AAT	GGA	TCT	GAC	TGC	CCG	GAC	AAG	TTT	TGC	TTA	TTC	CAG	TCT	GAA	ACC	1968
250	Asn	Gly	Ser	Asp	Cys	Pro	Asp	Lys	Phe	Cys	Leu	Phe	Gln	Ser	Glu	Thr	
251			625					630					635				
252																	
253	AAA	AAC	CTT	CTG	TTC	AAT	GAC	AAC	ACT	GAG	TGT	CTG	GCC	AGA	CTC	CAT	2016
254	Lys	Asn	Leu	Leu	Phe	Asn	Asp	Asn	Thr	Glu	Cys	Leu	Ala	Arg	Leu	His	
255		640					645					650					
256																	
257	GGC	AAA	ACA	ACA	TAT	GAA	AAA	TAT	TTG	GGA	CCA	CAG	TAT	GTC	GCA	GGC	2064
258	Gly	Lys	Thr	Thr	Tyr	Glu	Lys	Tyr	Leu	Gly	Pro	Gln	Tyr	Val	Ala	Gly	

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